

### **Amendments to the Claims**

**1. (Original)** A  $\beta$ -fructofuranosidase variant consisting of the following amino acid sequence:

- (a) a mutated amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues at positions 62, 122, 128, 165, 221, 395, and 550, or
- (b) a mutated homologue of the amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues corresponding to the amino acid residues at positions 62, 122, 128, 165, 221, 395, and 550 of SEQ ID NO: 2.

**2. (Original)** The variant according to claim 1, wherein the mutation is a substitution.

**3. (Currently amended)** The variant according to claim 2, wherein the substitution is

a substitution of the amino acid residue at position 62 with an acidic amino acid selected from the group consisting of aspartic acid and glutamic acid;

a substitution of the amino acid residue at position 122 with an amino acid selected from the group consisting of methionine, isoleucine, leucine, and valine;

a substitution of the amino acid residue at position 128 with an amino acid selected from the group consisting of asparagine and glutamine;

a substitution of the amino acid residue at position 165 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 221 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 395 with an amino acid selected from the group consisting of leucine, methionine, isoleucine, and valine; ~~and~~ or

a substitution of the amino acid residue at position 550 with a hydroxy amino acid selected from the group consisting of serine and threonine.

**4. (Original)** The variant according to claim 1, 2, or 3, which further has a mutation in at least one amino acid residue at positions 170, 300, 313, and 386 of the amino acid sequence represented by SEQ ID NO: 2 and its homologue.

**5. (Original)** The variant according to claim 4, wherein the mutation is a substitution.

**6. (Currently amended)** The variant according to claim 5, wherein the substitution is

a substitution of the amino acid residue at position 170 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 300 with an amino acid selected from the group consisting of tryptophan, phenylalanine, tyrosine, and valine;

a substitution of the amino acid residue at position 313 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine; ~~and~~ or

a substitution of the amino acid residue at position 386 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine.

**7. (Currently amended)** The variant according to claim 4, ~~5, or 6,~~ which has mutations in the amino acid residues at positions 165, 300 and 313.

**8. (Original)** The variant according to claim 7, wherein the mutations are substitutions.

**9. (Original)** The variant according to claim 8, wherein the substitutions are

a substitution of the amino acid residue at position 165 with an aromatic amino acid selected from the group consisting of tryptophan, phenylalanine, and tyrosine;

a substitution of the amino acid residue at position 300 with an amino acid selected from the group consisting of tryptophan, phenylalanine, tyrosine and valine; and

a substitution of the amino acid residue at position 313 with a basic amino acid selected from the group consisting of lysine, arginine, and histidine.

**10. (Original)** A  $\beta$ -fructofuranosidase variant consisting of the following amino acid sequence:

(c) a mutated amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues at positions 40, 379, and 381, or

(d) a mutated homologue of the amino acid sequence of SEQ ID NO: 2, which has at least one mutation in amino acid residues corresponding to the amino acid residues at positions 40, 379, and 381 of SEQ ID NO: 2.

**11. (Original)** The variant according to claim 10, wherein the mutation is a substitution.

**12. (Currently amended)** The variant according to claim 11, wherein the substitution is

a substitution of the amino acid residue at position 40 with an acidic amino acid selected from the group consisting of aspartic acid and glutamic acid;

a substitution of the amino acid residue at position 379 with cysteine; ~~and~~ or

a substitution of the amino acid residue at position 381 with an amino acid selected from the group consisting of methionine, isoleucine, leucine, and valine.

**13. (Currently amended)** A polynucleotide encoding the  $\beta$ -fructofuranosidase variant of ~~any one of claims 1 to 12~~ claim 1 or 10.

**14. (Original)** A recombinant vector comprising the polynucleotide of claim 13.

**15. (Original)** A transformant comprising the recombinant vector of claim 14.

**16. (Currently amended)** A method for producing a fructooligosaccharide, which comprises the step of bringing the transformant of claim 15 or the  $\beta$ -fructofuranosidase variant of ~~any one of claims 1 to 12~~ claim 1 or 10 into contact with sucrose.